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Restriction Map of the RSV G Gene

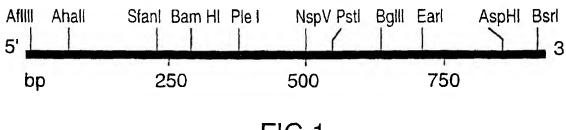


FIG.1



FIG.2A

55	AAG ACC	Lys Thr	
46	A CITA GAA	r Leu Glu	
37	CT AAG ACA	Ala Lys Thr	
	CGC ACC (Arg Thr A	
28	CAA	Asp Gln	
19	AAC	Asn Lys	
	<u>1</u>	: Ser Lys	
10	TICCAAAC ATIG	Met	

109	TA AAT	eu Asn	
100	TA TAT AAG I	eu Tyr Lys Leu Asn	
	. GGC T	: Ile Ser Ser Gly Leu	
91	133	Set	
	47	Ser	
	ATA	11e	
82	\mathcal{L}	Щ	
	TTA	Lea	
	TIA TIA TIC	Leu	
73	GAT	His	
	IC AAT CAT TTA TTA TI	Asn	
	ACT CTC	Leu	
64	ACT	Thr	
	SAC SAC SAC SAC SAC SAC SAC SAC SAC SAC	Asp	
	100	dīL	

	C TCA ACT	Ser	
154	ATG ATTA ATTC	t Ile Ile	
	3 GCA AII	1 Ala Met	
145	ATT CTG GCA	Ile Le	
136	TITA TOC	Leu	
	ATC ACA	lle Thr	
127	CAA	Gln	
~	TCT GTA GCA	r Val Ala	
118	CIT AAA ICI	Leu Lys Ser	
	5	Ľ	

217	AAA GTC ACA	Val Thr
	AAA G	His Lys Va
208	8	
	AAC (Asn
	80 17	Ser Ala
199	32	Ser
	8	Ala
	ATA	IIe
190	TEC	Phe
	ATA	Ile
	ATC.	Ile .
181	8	Ala
	ACA	Thr Ala
	ATT	Ile
172	ATA	Ile
	TCA CTT ATA	Lea
	TCA	Ser

271	8	Pro
	ACC	Thr
	ACA ACC	큠
262	AAC	Asn
	AAG	Liys
	AIIC	Пе
253	5	臼
	AGC	%
	ACA	Thr
244	GCA ACA AGC	Ala
	GAT	Gln Asp
	SA SA	Gln
235	ATTA	Ile
	GCA AIC	ı Ile
	8	Thr Ala
226	ACT (Thr
	ACA A	Leu Thr'
	CIPA	Let

325	CITY GGA AIC AGC TIC TCC AAT CIG TCT GAA	r Glu
	10 TC	왕 왕
316	AT C	Asn Le
(*)	100	Ser 7
	TIC	Page 1
307	AGC	Se R
	, AIC	. Ile
	£.	1 Gly
298	E	Lec
	CAG (् दिरि
•	5	Gln Asp Pro G
289	9	1 Asg
	F G	r Gh
0	CAC	u Th
280	E 2	r Le
	Y TA	Thr Tyr Leu Thr
	AC	E



FIG.2B

352 CTA GCT TCA ACA ACA CCA GGA GTC AAG TCA Leu Ala Ser Thr Thr Pro Gly Val Lys Ser 406 406 407 407 408 407 408 408 408 408 408 408 408 408 408 408		OC ARCEL	E.				
361 361 362 363 364 364 364 364 364 365 367 367 368 369 369 369 369 369 369 369 369 369 369	*\ }		595 AAG Lys	541 AAC Asn	487 AAT Asn	433 CAA Gln	379 TCA Ser
361 361 362 363 364 364 364 364 364 366 366 367 367 368 369 369 369 369 369 369 369 369 369 369		Lys	GGA Gly	AGC Ser	CCC Pro	ACA	AAG Lys
361 361 362 363 364 364 364 364 364 366 366 367 367 368 369 369 369 369 369 369 369 369 369 369		AAA Liys	CCA Pro	10c Cys	AAA Liys	CAA Gln	GIC
361 CA ACA ACA Ser Thr Thr 415 AAC ACA ACA ASTA ACA ASTA ACA ASTA ACA ASTA CAA CAA CAA CAA CAA CAA CAA CAA CAA CA		9 & Fi	586 AAA Ilys	532 ATA Ile	478 AAC Asm	424 ACC Thr	370 GGA Gly
361 CA ACA Ser Thr Ser Thr 415 VAC AAA VAC AAA VAC AAA CCA CLIP Pro 631 VAC TICC CLIP Pro CLI		ACA Thr	AAA Liys	AGC Ser	CCA Pro	ACA Thr	CCA Pro
361 CA ACA Ser Thr Ser Thr 415 VAC AAA VAC AAA VAC AAA CCA CLIP Pro 631 VAC TICC CLIP Pro CLI		AAG Liys	AAC Asm	13c Cys	A S	ACA Thr	ACA
OCT TCA Ala Ser Aba Aba Aba Caa Aba Gln Asm TTT GTA Acta Atta Acta Acta TTTT GTA Acta Atta Acta Atta Acta Acta Pro Thr		631 TTC Phe	577 CCA Pro	523 ccc Pro	469 AAA Lys	415 ACA Thr	361 ACA Thr
Acta Acta Acta Acta Acta Acta Acta Acta		ACC Iffir	ATA 11e	GTA Val	AAC Asm	AAC Asn	77.3 Ser
		Pro Pro	AGA Arg	TTT Phe	CAA Gln	AAA Lys	GCT Ala
352 CTA Leu 406 ACT Thr Thr Thr ASD ASD ASD ASD ASD ASD ASD ASD ASD ASD		622 AAA Lys	568 AAA Lys	514 AAC Asn	460 CGC Arg	406 ACT Thr	352 CTA Leu
AITA 111e 11Je 11Je 11Je 11Je 11Je 11Je 11J		AAA Lys	13C C/vs		CAA Gln	AAG Lys	ATA Ile
343 ACC ACC Thr Thr 397 ACA GTC Thr Val 451 ACA AAA Thr Lys 505 GAA GTG Glu Val 559 GCT ACC Ala 11e 613 CCT ACA		ACA 17hr	AIC 11e	GIG	AAA Lys	GIC	ACC
343 343 350 365 365 365 365 365 365 365 365 365 365		613 CCT Pro	559 GCT Ala	505 GAA Glu	451 ACA Ifhr	397 ACA Thr	343 ACC Thr
Cay ACC Gln Thr CCC ACA Pro Thr CAC TTC CAC TT		AAG Liys	13G Trp	TTC	ACT	ACA	ACC
HE KS DR KS BR		ACC Thr	연역	₹ <u>'</u>	당 없	CCC	CAA
334 334 388 388 388 308 309 442 442 442 496 7177 9177 9177 9177 9177 9177 9177 91		604 ACC Thr		496 TTT Phe		388 CAA Gln	334 TCA Ser
THE RESERVE THE THE THE THE THE THE THE THE THE TH		ACC		GAT	AGC	CTG	ACA Thr
ATTT 11e 11e ASTN ASTN ASTN ASTN ASTN ASTN ASTN ASTN		AAA Liys	AAT	AAT Asn	25 27 27 37	AAC	AIT Ile

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FIG.2C

for the state of t

And the property of the R. And H. H. Strain St. Strain

CAG TAGITTATTAA AAAAAAAA

Gln

Thr Arg

Thr

Pro g 883

Pro

Glu

සි

ACA ACA

CCC AAC Pro Asn

ICI Ser

T Ser

GA

901

892

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GAA Glu AAC Asm ACC Thr 865 8 757 811 856 TCC GAG CAC Thr Thr TGA Ser ACA Glu His 8 Pro CIC His Leu Leu 2 AAG Lys 748 CTG (802 TTC Phe Seg Thr Thr ACC ACC ACA AGT CAA ATG GAA ACC Glu Thr ACA ACA Pro Thr Thr Thr Thr ACT ACA 685 CC . 847 TCC. ACA Thr Ser Thr Gly Asn Pro Lys Leu Thr Ser Gln Met 739 793 Gln Thr Thr Lys Pro Lys Glu Val ACC AAA ACA AAC ATC . Ile Asn Thr Thr Lys Thr Asn Ile AAA OCA AAG GAA GIA TCT CAA GTC Gln Val Ser 784 838 Pro 766 AZA GGA AAT CCA AAA CTC 829 GC AAT CTA AGC CCT Gly Asn Leu Ser CAA ACC ACT A 721 AAC ACC ATC. Pro 712 ACC Thr GAA Glu 874 000 658 CCT 820 Lys B Pro Thr AAA ACC See See 333 GAG Leu Glu Ser

FIG.3A

			5 / 19)			
54 18	108 36	162 54	216 72	270	324 108	378 126	432 144
AAA GIC ACA CI'A ACA ACT GCA ATC ATA CAA GAT GCA ACA AGC CAG ATC AAG 54 Lys Val Thr Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr Ser Gln Ile Lys 18	OCA ACA TAC CTC ACT CAG GAT OCT CAG CTT GGA ATC AGC TTC TOC 108 Pro Thr Tyr Leu Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser 36	GAA ATT ACA TCA CAA ACC ACC ATA CTA GCT TCA ACA ACA CCA 162 Glu 11e Thr Ser Gln Thr Thr Thr 11e Leu Ala Ser Thr Thr Pro 54	GGA GTC AAG TCA AAC CTG CAA CCC ACA ACA GTC AAG ACT AAA AAC ACA ACA ACA 216 Gly Val Lys Ser Asn Leu Gln Pro Thr Thr Val Lys Thr Lys Asn Thr Thr Thr 72	ACA CAA CCC AGC AAG CCC ACT ACA AAA CAA CGC CAA AAC AAA CCA CCA 270 Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro 90	AAT AAT GAT TIT CAC TIC GAA GIG TIT AAC TIT GIA CCC TGC AGC 324 Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser 108	AAC AAT CCA ACC TGC TGG GCT ATC TGC AAA AGA ATA CCA AAC AAA 378 Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys 126	AAA CCA GGA AAG AAA ACC ACC ACC AAG CCT ACA AAA AAA CCA ACC TTC AAG ACA 432 Lys Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys Thr 144
GIC	ACC	Zer Ser	AAG '	ACA (AGC .	GGA GLy
AAA (Lys 1	AAC ACA ACC (Asn Thr Thr I	CIG	GIC A	CAA A	AAA CCC Lys Pro	ATA TGC AGC Ile Cys Ser	CCA C
CAC	AAC Asm	AAT (GGA (ACC (Thr (AAC 7	ATA 1	AAA (Liys

FIG.3B

there are it that there tout with him

Anth 47th Sain goth H. 48th H.

6/19 486 162 648 216 198 540 180 594 699 232 ACC Thr ACA CA ACA Thr ACC Thr Thr ACC 캶 멾 GAA Glu ACA CA Thr ACT TAG Pro gThr ACA AIG CAG Gln Met 333 Ser Gh Ile CAA GITA AIIC Arg Glu Val GIC Val 8 GAA Asn GAA Gln AAC AGI Set ACA 1117 AAG (Lys ACA Thr ACA Thr Thr TCT Ser AGA B Pro S Lyzs AAA Asn CICPro Lys Leu 5 Pro AAC Lys AAA ACC Thr AAA Pro Leu Ser 8 CTA AGC ACT Thr Thr Pro 8 ACC CC SPA PA ACC Thr Asn AAT AAC GGA AAT Gly Asn Gly Asn Set Gln GA. Ile ATC 8 Z Z Se K Pro CT Thr Thr GAA Glu ACC ACA Pro gAAA Liys Pro 8 ACC Thr Ser Gln 193 GAA CIC 9 Glu Asp Leu AAC Asn Asn 3 Set TG PG Ser GAT GAA Glu AAC Pro SP ACC Thr AAA Lys Thr Thr His ACA ACC 17 17 Ser CAC Lys AAA Pro Leu 8 CIC CAC His GAG Glu ACC Thr AAG Lys CIG Leu TIC 333 Ser

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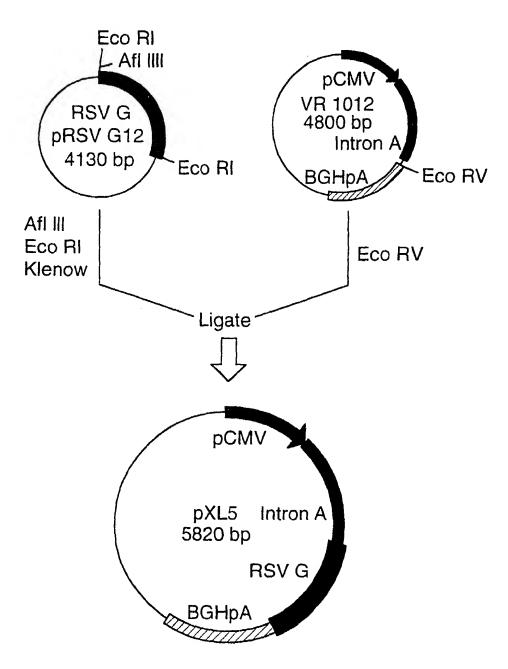


FIG.4.

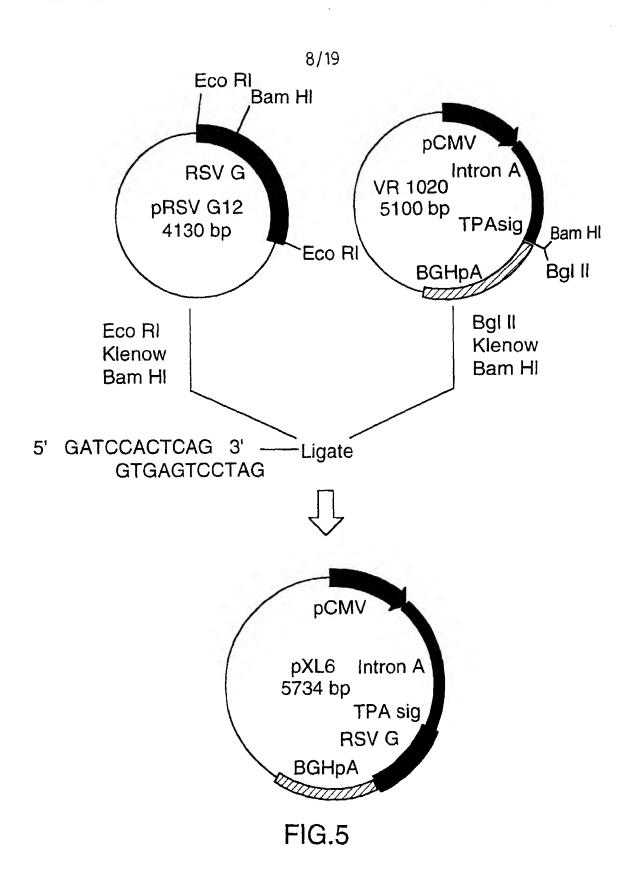


FIG.6A

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70	140	210	280	350	420	490	560
CAGCITIGICT	1000000106	CCGCACAGAT	TCATAATATG	TATTAATAGT	CGGTPAAATGG	CATAGTAACG	GCAGTACATC
60	130	200	270	340	410 420	480	550
GAGACGGICA	TTGCCGGGTG	GIGICAAAIA	TGTAICCAIA	ATTGACTAGT	ACATAACTITA COGTAAATGG	CGINIGITICC	TGCCCACTTG
20 30 40 50 60 70 GAITGAC GGIGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT	120 TCAGCGGGTG	190 ACCATATGCG	240 250 260 270 280 AICAGAITIGG TIGGATAGGI TGIAICCATA TCATAATATG	310 320 330 340 350 TCCAACAITYA CCGCCAIGIT GACAITIGAIT AITIGACIPAGI TAITIAAITAGI	400 GTTCCGCGTT	460 470 480 cccattgagg tcaataatga	540 TACGGTAAAC
40	110	180	250	320	390	460	530
TCTGACACAT	TCAGGGCCCC	CTCAGAGICC	CTATTGGCCA	CCGCCAIGIT	CATATATGGA	CCCATTGACG	GIGGAGIAIT
30	100	170	240	310	380	450	520
GGTGAAAACC	GACAAGCCCG	GCAGAITGEA	ATCAGATTGG	TCCAACAITA	GITCATAGCC	ACCACCCCC	ACCICAAIGG
20 CGGTGATGAC	80 90 100 110 120 130 140 GTAAGCCCAT GCCGCCA GACAAGCCCG TCAGGCCGGCTC TCAGCCGGCTC TTGGCGGGTC TCGGGGCTCG	150 160 170 180 190 200 210 CITAACIATG CGCCATCAGA GCAGAITGTA CTGAGAGTCC ACCATATGCG GTGTGAAATA CCGCACAGAT	230 ATACCCC	290 300 TACAITIMIA TIGGCICAIG	360 370 380 390 400 AAIICAAITAC GGGGICAITA GITICATAGCC CATATAIGGA GITICGGGTT	430 440 CECCTESC TEACCECCCA ACEA	500 510 520 530 540 550 CCAATAGGGA CTITICCATIG AGGICAAIGG GIGGAGIAIT TACGGIAAAC IGCCCACTIG
10	80	150	220	290	360	430	500
103033111 (33)	GIYAAGCGGAT	CITPACIAIG	GCCTAAGGAG AAAA	TACAITIAIA	AATCAATTAC	ccccccrcac	CCAATAGGGA

G.6B

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630	700	770	840	910	980	1050	1120
GCCATTATGC	TATTACCATG	CCAAGICICC	GICGIAACAA	AGCICGITITA	CGGGACCGAT	TPAGTPACCGC	GGCCTATAC
620	690	760	830	900	970	1040	1110
TGGCCCGCCT	TAGTCATCGC	ACGGGGAITIT	TTTCCAAAAT	ATATAAGCAG	TAGAAGACAC	AAGAGIGACG	TITIGGCITG
610	670 680 690	740 750	820	890	950 960 970	1020 1030 1040 1050	1090 1100
TCACCCTAAA	TIGGCAGIAC AICTACGIAT TAGICAICGC	CGIGGAIAGC GGITITGACTC	TCAACGGGAC	TGGGAGGICT	GCIGIT TIGACCICCA TAGAAGACAC COGGA	GAACGCGGAT TCCCCGTCCC AAGAGTGACG TAAGTACCGC	TCITATGCAT GCTATACIGT
600	670	740	810	880	(**)	1020	1090
TTCACCTCAA	TIGGCAGIAC	CGTGGATAGC	GGCACCAAAA TCAA	GCCTICTIACGG		GAACGCGGAT	TCTTATGCAT
590	650 660 ratioctac	730	800	870	940	1010	1080
ACCCCCCTA		CATCAATGGG	AGTITIGITITI	TGGGCGGTAG	GAGACGCCAT CCA	CGGIGCAITIG	CCCTITIGAC
570 580 590 600 610 620 630 AGTICIACCIANA TICACCICAA TICACCICAA TICACCICAAA TICACCICAAA TICACCICAAA TICACCICAAA TICACCICAAAA TICACCICAAAA TICACCICAAAA TICACCICAAAA TICACCICAAAAA TICACCICAAAAAAAAAA	650	710 720 730	790	850 860 870 880 890 900 910	930	1000	1060 1070
	ACCITATIGGG	GICATGCGGT TTTGGCAGTA CATCAATGGG	ANTGGG	CICCGCCCCA TICACGCAAA IGGGCGGIAG GCGIGIACGG IGGGAGGICT ATATAAGCAG AGCICGITTA	AGAICGCCIG GAGA	3 33 53	CTATAGACTC TATAGGCACA
570	640	710	780	850	920	990	1060
AAGIGIAICA	CCAGTACATG ACCTI	GTGATGCGGT	ACCCCATTGA CGTCA	CICCGCCCA	GIGAACCGIC AGAIK	CCAGCTTCCG CGGC	CTATAGACTC

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-1G.6C

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1190	1260	1330	1400	1470	1540	1610	1680
ACCAITAITG	CAACTAICIC	GGATGGGGTC	ATTAAACATA	CGGCGGAGCT	CICCIAACAG	TCCCCTIMAC	TRAGGCAGCG
1180	1250 1260	1320 1330	1380 1390 1400	1460	1530	1580 1590 1600	1660 1670 1680
TGGGTTATTG	CICITIGCCA CAACIAICIC	TATTITIPACA GGATGGGGTC	CCCCCGIGCC CCCAGITITI AITBAACATA	TCTCCGGTAG	CAGCTCCTTG	CCACCACCAC CAGIGIGCCG CACAAGGCCG	GCTGACGCAG ATGGAAGACT TAAGGCAGCG
1170 CCIMIAGGIG	1240 CATAACATGG	1310 ACGGACTICTG		1450 CATGGGCTCT	1520 GETUGCTUGG	1590 CAGIGIOCCG	
1160	1230	1300	1370	1440	1500 1510		1650
TATAGCTTAG	ATTACTAATC	AGAGACTGAC	ACAACGCCGT	GIGITICCGGA	CCATGCCTCC AGGGGCTCAT		GGCTCGCACG
1150	1220	1280 1290 1300 1310	1350 1360 1370	1420 1430	1500	1570	1640
TAGGTGATGG	GATACTTTCC	GCCAATAC TCTGTCCTTC AGAGACTGAC ACGGACTCTG	CAAATT CACATATACA ACAACGCCGT	33CCAA TCTCGGGTAC	CCATGCCTCC	AGCACAATGC	GIGGAGAITG
1130 1140 1150 1160 1170 1180 1190 ACCCCCCCTT CCTTATGCTA TAGGICATGS TAIPACCTTAG CCTATAGGIG TGGGTTATTG ACCALTATIG	1210 1210 ACCACTCCCC TAITTGGTGAC		1350 TTTACAAATT		1490 AGCCTGGTC	1550 1560 1570 IGGAGGCCAG ACTITAGGCAC AGCACAATGC	1620 1630 GIAIGICIC GAAAAIGAGC
1130	1200	1270	1340	1410	1480	1550	1620
ACCCCCCCTT	ACCACTCCCC	TATTGGCTAT AD	CCATTITAITA TITIM	COSTOCIATO TOCA	TCCACATCCG AGCO	TGGAGGCCAG	GIATGIGICT

FIG.6D

gering beite de te eine eine gering ode geine gering bie de freie gering beite gering beite gering gering gering Kande in de Kalled den Stadt welle tradt ift deuts in deuts in deuts gest deuts deuts deuts

			12 / 10				
1750	1820	1890	1960 R	2030	2100	2170	2240
GITGCGGIGC	GACATAATAG	CGIGIGAICA	CAGOCATOTG &	CCTAATAAAA	GCAGGACAGC	ACCCAGGIGC	ACACACCCTG
1730 1740 AAGAGICAGA GGIAACICCC	1800 1810 1820 TOCTGCCGCG COCOCCACCA GACATAATAG	1850 1860 1870 1880 1890 TCCTITICCAT GGGICTITIC TGCAGICACC GICGICGACA CGIGIGATCA	1940 1950 CIGCIGIGCC TICINGING	2020 2010 2020 CCTTCCTTGA CCCTGGAAGG TGCCACTCCC ACTGTCCTTTT	2090 GTGGGGTGGG	2140 2150 2160 2170 carderigas arceassise	2230 CITCICIGIG
		1870 TGCAGICACC	1940 CTGCTGTGCC	2010 TGCCACTCCC	2080 ATTCTGGGGG	2150 ATCCCGTCGC	2220 GCCACATCCC
1710 1720	1790	1860	1930	2000	2070		2200 2210 2220
CIGAGITIGIT GIATICIGAL	CAGTACTICGT	GGGICTITIC	GGATCCAGAT	CCCTGGAAGG	GIGICALICE		TCCTGGGCCA GAAAGAAGCA GGCACATCCC
1710	1780		1920	1990	2060	2130	2200
CICAGITICIT	GIAGICIGAG		CCAGGCGCCT	CCITCCITGA	GICTGAGIRG	CAATAGCAGG	TCCTGGGGCCA
1690 1700 GCAGAAGAAG ATGCAGGCAG	1760 1770 TGITTAACGGT GGAGGGCAGT	1830 1840 CTGACAGACT AACAGACTGT	1900 1910 1920 1930 1930 GAITAICGCGG CCGCTCTAGA CCAGGCGCCT GGAITCCAGAT	1970 1980 TIGITIGOCC CICCCCGIG	2040 2050 2060 2070 2080 TCAGGAAATT GCATCGCATT GTCTGAGTAG GTGTCATTCT ATTCTGGGGG	2110 2120 2130 2130 AAGGGGGAGG ATTGGGAAGA CAATAGCAGG	2180 2190 TCAAGAATTG ACCCGGTTCC
1690	1760	1830	1900	1970	2040	2110	2180
GCAGAAGAAG	TGTTPACCGGF	CTGACAGACT	GATATCGCGG	TTGTTTGCCC	TGAGGAAAIT	AAGGGGGAGG	TCAAGAAITG

FIG.6E

er eine gering er is dem einer gering i de geme de gering is de gemen gering demig de gemen de gemen de gemen de gemen de gemen de gemen gemen gemen gemen gemen Raud auf El timb fence Analt seite taute tel bigt trigt bradt sond bradt timb

		1	3 / 19				
2310	2380		2520	2590	2660	2730	2800
TCCCCTTCA	ACCTAGCCTC		OCTCGGTCGT	AGGGGATAAC	TTGCTGGCGT	GGCGAAACCC	TCCGACCCTG
2300	2370 2380	2440	2510	2580	2650	2690 2700 2710 2720 2730 cercaceace arcacaaaa regaceeceace	2790
TCAGGAGGGC	ACCAAACCAA ACCTAGCCTC	AGAAAATGCC	GACTEGETGE	CCACAGAATC	AAAGGCCGCG		Geteteeter
2270 2280 2290	2360	2430	2500	2560 2570	2640	2710	2780
TTCCAGCCC ACTCATAGGA CACTCATAGC	TCAITCAGCCC	GCACAGGGAG	CICGCICACT	AAAGGCGGTA ATACGGTTAT	GGAACCGIDA	TOGACOCTICA	TCCCTCGTGC
2280	2350	2420	2490		2630	2700	2770
ACTCATAGGA	TCTCCCTCCC	GCTATTAAGT	CITCCGCITC		CAAAAGGCCA	ATCACAAAAA	CCCIGGAAGC
	2340 TGGAGCGGTC	2410 AGCAAGATAG	2480 CATAGAAITIT	2550 CAGCICACIC	2620 AAAAGGCCAG		2760 AGGCGITICC
2250 2260 TCCACGCCCC TGGITCTTAG	2320 2330 ATCCCACCC CTAAAGTACT	2390 2400 2410 2420 2430 2440 2450 CAAGAGIGGG AAGAAAITAA AGCAAGAIAG GCIAITIAAGI GCAGAGGGAG AGAAAAIGCC TCCAACAIGI	2460 2470 GAGGAAGTAA TGAGAGAAAT	2530 2540 TCGCCTCCGC CGAGCCGTAT	2600 2610 2620 2630 2640 2650 2660 GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAAGGCCA GGAACCGTAA AAAGGCCGCG TTGCTGGCGT	2670 2680 TITICCATAG GCICCGCCC	2740 2750 2760 2770 2780 2790 2800 GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCTG
2250	2320	2390	2460	2530	2600	2670	2740
TCCACGCCCC	ATCCCACCC	CAAGAGTGGG	Gaggaagtaa	TCGCTGCG	GCAGGAAAGA	TITICCAIRG	GACAGGACTA

FIG 6F

			14 / 19				
2870	2940	3010	3020 3030 3040 3050 3060 3070 3080 $\frac{\pi}{5}$ GCAGCCACTIG GIAACAGGAT TAGCAGAGG AGGIATGTAG GCGGTGCTAC AGAGTTCTTIG AAGTGGTGGC $\frac{\pi}{6}$	3150	3220	3290	3360
TCACGCTGTA	TTCAGCCCGA	GCCACTGGCA		CCTTCGGAAA	TTGCAAGCAG	GACGCTCAGT	ACATCCTTTT
2840 2850 2860 2870 CCTTICGGGAA GCGIGGCGCT TTCTCATAGC TCACGCTGTA	2920 2930	3000	3070	3130 3140	3210	3280	3350
	CTGTGTGCAC GAACCCCCG	ACGACTITATC	AGAGITICITIG	CECTICTICCTIC AAGCCAGTTA	GFFFFFFGF	TACGGGGTCT	ATCTTCACCT
2850	2920	2990	3060	3130	3200	3270	3340
GCGIGGCGCT	CIGIGIGCAC	CCGGTAAGAC	GCGGTGCTPC	CECTCTECTE	GGTAGCGGTG	TGATCITITIC	ATCAAAAAGG
2840	2910	2980	3050	3120	3180 3190	3260	3330
CCTTCGGGAA	CCAAGCTGGG	TGAGICCAAC	AGGTATGTAG	TIGGIAICIG	CCGGCAAACA AACCACCGCT	GAAGAICCIT	TCAIGAGAIT
2830	2900	2970	3040	3110	_	3250	3320
CCCCTTTCTC	GICGITCGCT	ACTATCGICT	TAGCAGAGCG	AGAACAGTAT		AGGAICICAA	GGGAITTIGG
2810 2820 CCCCTTACCS GATACCTGTC	2880 2890 GGIPATCTCAG TTCGGTGTPAG	2950 2960 2970 2980 2990 3000 3010 COCTIGCOCC TITATICCOCTIA ACTATICGICT TGAGICCAAC CCGGTAAGAC ACGACITATIC GCCACTIGGCA	3030 GTAACAGGAT	3090 3100 3110 CIPACTPCGG CTACACTPGA AGAACAGTAT	3160 3170 AAGAGIIIGGI AGCICIIIGAI	3230 3240 3250 3260 3270 3280 CAGAITIAGGC GCAGAAAAA AGGAICICAA GAAGAICCIT IGAICITITIC TAGGGGGICT	3300 3310 3320 3330 3340 3350 3360 GGAACGAAAA CIGACGITAA GGGAITTIGG TCAIGAGAIT AICAAAAAGG AICTICACCT AGAICCTITT
2810	2880	2950	3020	3090	3160	3230	3300
CCCCTTPACCG	GGIMICICAG	CCGCTGCGCC	GCAGCCACTG	CIPACTACGG	AAGAGTIGGI	CAGAITTACGC	GGAACGAAAA

FIG.60

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			15/19				
3430	3500	3570		3710	3780	3850	3920
TTACCAATGC	CTCGGGGGGG	CCCCATCATC		TCAGCAAAAG	CAACCAAITA	GGATTATCAA	ATAGGATGGC
3420 3430	3480 3490 3500	3560	3630	3690 3700 3710	3770 3780	3840	3910
GGICTGACAG TTACCAATGC	GITCAICCAT AGITGCCIGA CICGGGGGG	GCCTGAATCG	ACCAGTTGGT	GCGTGATCTG ATCCTTCAAC TCAGCAAAG	GCCAGIGITA CAACCAAITA	ATTCATATCA	AGGCAGITCC
3410	3480	3550	3620	3690	3760	3830	3900
GAGIDAAACIT	GITCAICCAI	CICATACCAG	TTGTAGGTGG	GCGTCATCTG	GIPATGCICT	ACTGCAATIT	AAACTCACCG
3400	3460 3470	3540	3610	3680	3750	3820	3890
AAGTATATAT	CICAGCGAIC IGICIAITIC	GIGITIOCICA	GAGAGCTITIG	TCGGGAAGAT	TCAAGICAGC	ATCAAATGAA	ATCAAGGAGA
3390		3530	3600	3670	3740	3810	3880
AATCAATCTA		CGTCAAGAAG	CACGGITGAT	GICIGCGITG	CGCCGTCCCG	CICAICGAGC	CETTICTISTA
3370 3380 3390 3400 3410	3440 3450	3510 3520 3530 3540 3550 3560 3570	3580 3590 3600 3610 3620 3630 3640	3650 3660 3670 TITITIC CCACGGAACG GICTICCGTTG	3720 3730	3790 3840 3850 3820 3830 3840 3850	3860 3870 3880 3890 3900 3910 3920
AAATTAAAAA TGAAGITITTA AATCAAICITA AAGITATAITA GAGITAAACITT	TTAATCAGIG AGGCACCIAI	GGGGGCCTG AGGICTGCCT CGTGAAGAAG GTGTTGCTGA CTCATACCAG GCCTGAATCG CCCCATCATC	CAGCCAGAAA GIGAGGGAGC CACGGITGAT GAGAGCTITIG TIGITAGGIGG ACCAGTIGGT GAITITIGAAC		TTCCATTTAT TCAACAAGC	ACCAATTGIG ATTAGAAAA CICATCGAGC AICAAATGAA ACTGCAATTT ATTCATATCA GGATTAICAA	TACCATATIT TIGAAAAAC CGITICIGIA AIGAAGAGA AAACICACC AGGCAGITC AIAGGAIGC
3370	3440	3510	3580	3650	3720	3790	3860
AAATTAAAAA	TTAATCAGIG	GGGGGCGCTG	CAGCCAGAAA	TTTTCCTTTC	TICCAITIAI	ACCAAITIGIG	TACCATATIT

FIG.6F

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4060	4130	4200 g	4270	4340	4410	4480
AAAAGCITAT	CATCAACCAA	ACAATTACAA G	GAATCAGGAT	CATCAGGAGT	CAICICAICT	TTCCCATACA
4050	4120	4190		4330	4400	4470
TGAGAATGGC	AAAICACICG	TGITTAAAAGG		AACCATGCAT	TTAGICIGAC	CGCATCGGGC
4040	4110	4180	4250		4390	4460
CTGAATCCGG	CICGICAICA	ACCCCATCCC	CATCAACAAT		GTCAGCCAGT	ACAACTCTGG
4030	4100	4170	4240	4310	4380	4450
TGAGIGACGA	AGCCAITIACG	GAGACGAAAT	ACTGCCAGCG	CGGGGATCGC	CATAAATTCC	TGITTCAGAA
4020 GAAATCACCA	4090 TCAACAGGCC					4440 ACCITIGCCA
4010	4080	4150	4220	4290	4360	4420 4430 4440 4450 4460 GIRACAICAT IGGCAACGCT ACCITIGCCA IGITICAGAA ACAACTCIGG
TRICAAGIGA	CCAGACTIGI	ATTCGICAIT	AATGCAACCG	TACCIGGAAI	TOCTTGATGG	
4000	4070	4140	4210	4280	4350	4420
AAAATAAGGT	GCATTITCITIT	ACCGITTAITIC	ACAGGAATCG	AFFICITCEA	ACCCATAAAA	GTAACATCAT
	4010 4020 4030 4040 4050 TATICAAGTICA GAAATCACCA TGAGTIGACGA CTGAATCCGG TGAGAATGGC AAAAGC	4050 TGAGAATGGC AAAAGC 4120 AAATCACTGG CATCAA	4000401040204030404040504060AAAATAAGSTTGAGTGACGATGAGTGACGATGAGAATOCCA12041304070408040904100411041204130GCATTTCTTTCCAGACTTGTTCAACAGCCA6004170418041904200ACCGTTATTCA15041604170418041904200ACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCCATGAGTGTTAAAAAGGACAATTACAA	4020 4030 4040 4050 GAAAITCACCA TGAGIGAGGA CIGAAITCGG TGAGAAITGGC AAAAC TCAACAGGC AGCCAITTAGG CICGICAITCA AA190 A1100 41100 TCAACAGGC AGCCAITTAGG CICGICAITCA A4190 4190 A190 GCGCCTGAGC GAGACGAAAT ACGCGATCGC TGTTAAAAGG ACAATTI 4230 4240 4250 4260 GCGCCAGGAAC ACTGCCAGGG CATCCAACAAT ATTITTCACCT GAATCA	4020 4030 4040 4050 CAAATCACCA TGAGTGACGA CTGAATCCGG TGAGATGGC Aaaac 4090 4100 4110 4120 CATCAA TCAACAGGC AGCCATTACG CTCGTCATCA AaatCACTCG CATCAA 4160 4170 4180 4190 Acatca GCGCCTGAGC GAGACGAAAT ACGCGATCGC TGTTAAAAAGG ACAATTT 4230 4240 4250 4260 ACACCAACAAA ACACCAACCAACCAAAA ACACCAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAA	4020 4030 4040 4050 AAAAC CAAATCACCA TGAGTGACGA CTGAATCCGG TGAGAATGGC AAAAC 4090 4100 4110 4120 CATCAACAGCG CATCAACAGCG CATCAACAGCG CATCAACAGCG CATCAACAGCG ACAGCGATCGC TGTTAAAAAGG ACAGTGAATG 4230 4240 4250 4260 AAATCAACAGCG CATCAACAGAGT A330 A330 A330 A4400 4370 4380 4380 4380 4400 A100 A

FIG.61

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		47	7.140			
4550	4620	4690	4760 5	4830	4900	
AAICAGCAIC	GITCCTIGIA	AIGIAACAIC	GITAITGICT	ATTTCCCCGA	CGIAICACGA	
4540	4610	4680	4750	4820	4890	
TACCCATATA	GGCTCATAAC	ATCTTGTGCA	ATTITAICAGG	TTCCCCCCAC	TRAAAATAGG	
4530	4600 4610 4620	4670	4720 4730 4740 4750 4760	4810	4880	
AGCCCAITIPA	CGTTGAATAT GGCTCATAAC GFTCCTTGTA	ATATATTITT	TGGCTTTCCC CCCCCCCCA TTATTGAAGC ATTTATCAGG GTTATTGTCT	CAAATAGGGG	CAITTAACCTA	
4520	4590	4660	4730	4800	4870	
CATTATCGCG	AGACGITICC	GTTCATGATG	ccccccca	GAAAAATAAA	ATTAICAIGA	
4510	4580	4650	4720	4790	4860	
GATTGCCCGA	GCCTCGAGCA	CAGITITIAIT	133C1111CCC	AATCTATTTA	AGAAACCAITI	
4490 4540 4510 4520 4530 4540 4550 ACCCATATA PATCACCATC	4560 4570 4580 4590 CATIGGAA AGACGITTICC	4630 4640 4650 4660 4670 4680 4690 TIACIGITIA IGIAAGCAGA CAGITITIAIT GITCAIGAIG AIAIATITIT AICITIGIGCA AIGIAACAIC	4710 AGACALTITIG AGACACAACG	4770 4780 4790 4800 4810 4820 4830 CAICAGGGA TACATAITIG AATGIAITITA GAAAAATAAA CAAAIAGGGG TICCGCGGCAC AITITCCCCGA	4840 4850 4860 4870 4880 4890 4900 A900 AAAGIGCCAC CIGACGICIA AGAAACCAIT AITAICAIGA CAITIAACCIA TAAAAAIAGG CGIAICACGA	JI.
4490	4560	4630	4700	4770	4840	4910
ATCGATAGAT	CATGITIGGAA	TTACIGITITA	AGAGAITITIG	CATGAGGGGA	AAAGIGCCAC	GECCTITICS TC

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0/.	ACCTCTGCGA	140	GAAGAGAGGG	10	y C
09	TOGAGAGAAA	130	TOCATIOCAAT		
20	AGTCCAGGGC	120	GAAGCAATCA		CHACCE
40	ATCCTACAGG	110	GGGACGCTGT	180	CHESTON
30	CAGAGCIGAG	100	GICAAITITAA	170	GIRTIGGACA
20	CTGCAGTCAC CGTCGTCGAC CAGAGCTGAG ATCCTACAGG AGTCCAGGGC TGGAGAGAAA ACCTCTGCGA	90	SCAAAGGGAA GGAGCAAGCC GIGAAITITAA GGGACGCIGI GAAGCAAITCA IGGAIGCAAT GAAGAGAGG	160	
OT	CTGCAGTCAC	80	GGAAAGGGAA	150	CTCTGCTGTG

19/19

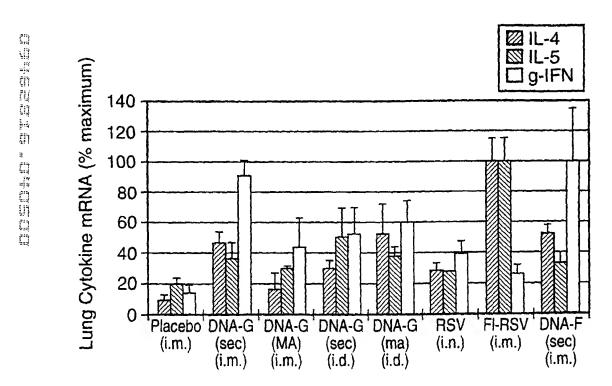


FIG.8